

# FIG. 1A

10 30 50  
 ECTGAAGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGGAGG  
 70 90 110  
 GACGCTCTTCTTCTGCCCCAGGGGTCCCTGGGCCGATGGGATCAGCAGAAAGAAATGCGAG  
 130 150 170  
 AGAAGCAGCCCTTTTGAGAAAGGAAGTCACTATCCCAGAGCCCCAGACTGAGCGGATGGAGTT  
 M E L  
 190 210 230  
 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA  
 R K Y G P G R L A G T V I G G A A Q S K  
 250 270 290  
 ATCACAGACTAAATCAGACTCAATCACAAGAGAGTTCCCTGCCAGGCCCTTTACACAGCCCC  
 S Q T K S D S I T K E F L P G L Y T A P  
 310 330 350  
 TTCCTCCCCGTTCCCCGCCCTCACAGGTGAGTGACCAACCAAGTGCTAAATGACGCCCGAGGT  
 S S P F P P S Q V S D H Q V L N D A E V  
 370 390 410  
 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCCTATGACTATGGAGAAAACGAGAGTGACTC  
 A A L L E N F S S S Y D Y G E N E S D S  
 430 450 470  
 GTGCTGTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACCTTCGACCGGGCCTTCCT  
 C C T S P P C P Q D E S L N F D R A F L  
 490 510 530

MATCH WITH FIG. 1B

# FIG. 1B

MATCH WITH FIG. 1A

GCCAGCCCTCACAGCCCTCCTTCTGCTGGGCTGCTGGCAACGGCGGTGGCAGC  
 P A L S L L F L L G L L G N G A V A A 590  
 550  
 CGTGTGCTGAGCCGGGACAGCCCTGAGCAGCACCAGACACCTTCTGCTCCACCTAGC  
 V L L S R R T A L S S T D T F L L H L A 650  
 630  
 610  
 TGTAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA  
 V A D T L L V L T L P L W A V D A A V Q 710  
 690  
 670  
 GTGGTCTTTGGCTCTGGCCTCTGCAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA  
 W V F G S G L C K V A G A L F N I N F Y 770  
 750  
 730  
 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTTCATGC  
 A G A L L L A C I S F D R Y L N I V H A 830  
 810  
 790  
 CACCCAGCTCTACCGCGGGGGCCCCCGCGGTGACCCCTCACCTGCCCTGGCTGTCTG  
 T Q L Y R R G P P A R V T L T C L A V W 890  
 870  
 850  
 GGGGCTCTGCTGCTTTTCGCCCTCCAGACTTCATCTTCTGTGCGCCACCCAGCAGA  
 G L C L L F A L P D F I F L S A H H D E 950  
 930  
 910  
 GCGCCTCAACGCCACCCACTGCCAATACAACCTCCACAGGTGGCGCCGACGGCTCTGCG  
 R L N A T H C Q Y N F P Q V G R T A L R

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

FIG. 1C

970 990 1010  
GGTGTGCAGCTGGTGGCTGGCTTTCTGTGCTGCCCTGCTGGTCATGGCCTACTGCTATGC  
V L Q L V A G F L L P L L V M A Y C Y A  
1030 1050 1070  
CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGGCCTGCGGGCCATGCGGGCT  
H I L A V L L V S R G Q R R L R A M R L  
1090 1110 1130  
GGTGTGGTGGTGGTGGCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGGCT  
V V V V V V A F A L C W T P Y H L V V L  
1150 1170 1190  
GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCCGAGAAAGCAGGGT  
V D I L M D L G A L A R N C G R E S R V  
1210 1230 1250  
AGACGTGGCCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACCTGCTGCCCTCAACCCGCT  
D V A K S V T S G L G Y M H C C L N P L  
1270 1290 1310  
GCTCTATGCCCTTTGTAGGGGTCAAGTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT  
L Y A F V G V K F R E R M W M L L L R L

3 / 6

MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

# FIG. 1D

1330 1350 1370  
GGGCTGCCCCAACAGAGAGGGCTCCAGAGGAGCCATCGTCTTCCCGGGGATTTCATC  
G C P N Q R G L Q R Q P S S R R D S S  
1390 1410 1430  
CTGGTCTGAGACCTCAGAGGCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC  
W S E T S E A S Y S G L \*  
1450 1470 1490  
TTTCGCCCAAGTCTGACTTCCCCCGCATTCAGGCTCCTCCCTCCCTGCGGCTCTGG  
1510 1530 1550  
CTCTCCCCAAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACACCAGTCTCCC  
1570 1590 1610  
GGGAAGCCACCCCTCCAGCTCTGAGGACTGCACCATTTGCTGCTCCTTAGCTGCCAAGCCCC  
1630 1650 1670  
CATCCTGCGCGCCGAGGTGGCTGCCCTGGAGCCCCCACTGCCCTTCTCATTTGGAAACTAAA  
1690 1710 1730  
ACTTCATCTTCCCCAAGTGC GGGAGTACAAGGCATGGCGTAGAGGGTGTGCCCCCATGA  
1750 1770 1790  
AGCCACAGCCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCCATGGTCCCCCAAGACCTCTAT  
1810 1830 1850  
ATTTGGTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAGATCG  
1870  
TCAGGAAAAAAAAA

## FIG. 2A

54 DHQVLNDAEVAALLNFSSSYDYGENESDSCCTSPPCQDFSLNFDRAFL 103  
 . . . . .  
 2 ESDSFEDFWKGEDLSNYSYSTLPFLDAAPEPE . . . . . SLEINKYFV 46  
 . . . . .  
 104 PAL<sup>4</sup>SLFLGLGNGAVAAVLLSRRTALSSD<sup>4</sup>TFLHLAVADTLLVLT<sup>4</sup>L 153  
 . . . . .  
 47 VIIYALVFLSLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALT<sup>4</sup>L 96  
 . . . . .  
 154 PLWAVDAAVQWVFGSLCKVAGALFNINFYAGALLACISFDRYLNIVHA 203  
 . . . . .  
 97 PIWAASKVNGWIFGTFCLKVVSLLKEVNFYSGILLACISVDRYLAIVHA 146  
 . . . . .  
 204 TQLYRRGPPARVTLTCLAVWGLCLL<sup>4</sup>FALPD<sup>4</sup>FI<sup>4</sup>LSAHHDERLNATHCQYN 253  
 . . . . .  
 147 TRTLTO.KRYLVKFICLSIWGLSLLALPVL<sup>4</sup>LFRRTVYSSNVSPACYEDM 195  
 . . . . .  
 254 FPQVG..RTALRVLQLVAGFL<sup>4</sup>LP<sup>4</sup>LLVMAYCYAHILAVLLVSRGQRRLLRAM 301  
 . . . . .  
 196 GNNTANWRMLLRILPQSF<sup>4</sup>GFIV<sup>4</sup>PL<sup>4</sup>LM<sup>4</sup>FCYGF<sup>4</sup>TL<sup>4</sup>RTLFKAHMGQKHRAM 245  
 . . . . .

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

[illegible]



VIA HAND DELIVERY MARCH 18, 2002

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

**SUBMISSION OF SUBSTITUTE FORMAL DRAWINGS**

Commissioner for Patents  
Washington, D.C. 20231

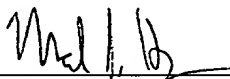
To the Official Draftsperson:

Applicants submit herewith Substitute Formal Drawings of Figures 1A-1D and 2A-2B (six sheets) to replace the previously filed drawings of Figures 1A-1D and 2A-2B (six sheets). The enclosed drawings have been amended to correspond to the sequences shown in the Substitute Sequence Listing filed herewith, as discussed in detail in the Response and Amendment also filed herewith.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: March 18, 2002

  
Mark J. Hyman (Reg. No. 46,789)  
Attorney for Applicants

**Human Genome Sciences, Inc.**  
9410 Key West Avenue  
Rockville, MD 20850  
(240) 314-1224

Enclosures  
KKH/MJH/KC/mlm

FIG. 1A

10 30 50  
CCTGAAGGAGAGCAGGGAGAGAGAGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG  
70 110  
GACGCTCTTCTTCTGCCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAGAATGCGAG  
130 150 170  
AGAAGCAGCCCTTTGAGAAGGGAAGTCACTATATCCAGAGCCCAGACTGAGCGGATGGAGTT  
M E L  
190 210 230  
GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA  
R K Y G P G R L A G T V I G G A A Q S K  
250 270 290  
ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCTCTGCCAGGCCCTTTACACAGCCCC  
S Q T K S D S I T K E F L P G L Y T A P  
310 330 350  
TTCTCTCCCGTTCCCGCCCTCACAGGTGAGTGACCAACCAAGTGCTAAATGACCGCCGAGGT  
S S P F P P S Q V S D H Q V L N D A E V  
370 390 410  
TGCCGCCCTCTCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTC  
A A L L E N F S S S Y D Y G E N E S D S  
430 450 470  
GTGCTGTACCTCCCGCCCTGCCCCACAGGACTTCAGCCTGAACCTTCGACCGGGCCTTCCT  
C C T S P P P C P Q D F S L N F D R A F L



FIG. 1B

490 510 530  
GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGGTGGCAGC  
P A L Y S L L F L L G L L G N G A V A A  
550 570 590  
CGTGCTGCTGAGCCGGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC  
V L L S R R T A L S S T D T F L L H L A  
610 630 650  
TGTAGCAGACACGCTGCTGGTGTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA  
V A D T L L V L T L P L W A V D A A V Q  
670 690 710  
GTGGGTCTTTGGCTCTGGCCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA  
W V F G S G L C K V A G A L F N I N F Y  
730 750 770  
CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCCGTACCTGAACATAGTTCATGC  
A G A L L L A C I S F D R Y L N I V H A  
790 810 830  
CACCCAGCTCTACCGCGGGGGCCCCCGCGGTGACCCCTCACCTGCCCTGGCTGTCTG  
T Q L Y R R G P P A R V T L T C L A V W  
850 870 890  
GGGGCTCTGCCCTGCTTTTCGCCCTCCACAGACTTCATCTTCCTGTGGCCCCACCGACGA  
G L C L L F A L P D F I F L S A H H D E

FIG. 1C

910  
GGCCCTCAACGCCACCCACTGCCAATAACAATTCCACACAGGTGGGCCGCACGGCTCTGCG  
R L N A T H C Q Y N F P Q V G R T A L R  
970 990 1010  
GGTGTGCAGCTGGTGGCTGGCTTTCTGTGCTGCCCTGCTGGTCATGGCCTACTGTATGC  
V L Q L V A G F L L P L L V M A Y C Y A  
1030 1050 1070  
CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCCCTGCGGCCATGCGGCT  
H I L A V L L V S R G Q R R L R A M R L  
1090 1110 1130  
GGTGGTGGTGGTGGCCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGCT  
V V V V V V A F A L C W T P Y H L V V L  
1150 1170 1190  
GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCCGCAACTGTGGCCGAGAAAGCAGGGT  
V D I L M D L G A L A R N C G R E S R V  
1210 1230 1250  
AGACGTGGCCCAAGTCGGTCACCTCAGGCCCTGGGCTACATGCACCTGCTGCCCTCAACCCGCT  
D V A K S V T S G L G Y M H C C L N P L  
1270 1290 1310  
GCTCTATGCCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT  
L Y A F V G V K F R E R M W M L L L R L

## FIG. 1D

1330 1350 1370  
GGGCTGCCCCAACAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTTCATC  
G C P N Q R G L Q R Q P S S R R D S S  
1390 1410 1430  
CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGAGAGCCGGAATCCGGGCTCCCC  
W S E T S E A S Y S G L \*  
1450 1470 1490  
TTTCGCCACAGTCTGACTTCCCCGCAATTCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG  
1510 1530 1550  
CTCTCCCCAATATCCTCGCTCCCGGACTCACTGGCAGCCCCAGCACCCAGGTCTCCC  
1570 1590 1610  
GGGAAGCCACCCCTCCAGCTCTGAGGACTGCACCATTTGCTGCTCCTTAGCTGCCAAGCCC  
1630 1650 1670  
CATCCTGCCGCCCGAGGTGGCTGCCCTGGAGCCCCCACTGCCCTTCTCATTTGGAAACTAAA  
1690 1710 1730  
ACTTCATCTTCCCCAAGTGCGGGAGTACAAGGCATGGCGTAGAGGTGCTGCCCCATGA  
1750 1770 1790  
AGCCACAGCCCGAGCCTCCAGCTCAGCAGTGA CTGTGGCCATGGTCCCCCAAGACCTCTAT  
1810 1830 1850  
ATTTGGTCTTTTATTTTATGTCTAAATCCTGCTTAAACTTTTCAATAAACAAAGATCG  
1870  
TCAGGAAAAA

# FIG. 2A

54 DHQVLNDAEVAALLNFSSSYDYGENESDSCCTSPPCQDFSLNFDRAFL 103  
 . . . . .  
 2 ESDSFEDFWKGEDLSNYSSSTLPPFLDAPCEPE . . . . .SLEINKYFV 46  
 . . . . .  
 104 PALYSLLFLLGLLGNGAVAAVLLSRRRTALSSTDTFLLHLAVADTLLVLTLL 153  
 . . . . .  
 47 VIIYALVFLSLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLL 96  
 . . . . .  
 154 PLWAVDAAVQWVFGSLCKVAGALFNINFYAGALLLACISFDRYLNIVHA 203  
 . . . . .  
 97 PIWAASKVNGWIFGTFCLCKVVSLKEVNFYSGILLLACISVDRYLAIVHA 146  
 . . . . .  
 204 TQLYRRGPPARVTLTCLAVWGLCLLLFALPDFIFLSAHHDERLNATHCQYN 253  
 . . . . .  
 147 TRTLTO.KRYLVKFICLSIWGLSLLALPVLLFRRTVYSSNVSPACYEDM 195  
 . . . . .  
 254 FPQVG..RTALRVQLVAGFLPLLV MAYCYAHILAVLLVSRGQRRLLRAM 301  
 . . . . .  
 196 GNNTANWRMLLRILPQSFGEIVPLLIMLFCYGFTRTLFKAHMGQKHRAM 245  
 . . . . .

## 5

[illegible]

RRVIFAVVLI FLLCWL PYNVLV LADTLM RTQVIQ ET CERRNHIDRA

[illegible]

ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVCG

[illegible]

SSSGHTSTT

VIA HAND DELIVERY MARCH 18, 2002

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

**STATEMENT UNDER 37 C.F.R. §§1.821 AND 1.825**

Commissioner for Patents  
Washington, D.C. 20231

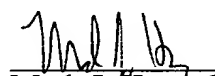
Sir:

Pursuant to 37 C.F.R. §§1.821(f) and 1.825(b), Applicants hereby certify that the sequence listing information recorded in computer readable form and submitted herewith is identical to the written (on paper) Substitute Sequence Listing submitted herewith.

Applicants further certify under 37 C.F.R. §§1.821(g) and 1.825(a) that the Substitute Sequence Listing submitted herewith contains no new matter.

Respectfully submitted,

Dated: March 18, 2002



Mark J. Hyman  
Attorney for Applicants

Reg. No. 46,789

**Human Genome Sciences, Inc.**  
9410 Key West Avenue  
Rockville, MD 20850  
Telephone: (240) 314-1224

Enclosures  
KKH/MJH/KC

# SEQUENCE LISTING

<110> Li, Yi  
 <120> Human G-Protein Chemokine Receptor HSATU68  
 <130> PF218US  
 <140> US 09/101,518  
 <141> 1998-12-21  
 <150> PCT/US96/00499  
 <151> 1996-01-11  
 <160> 9  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 1876  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (173)..(1420)  
 <223>  
 <400> 1  
 cctgaaggga gagcagggag agagaggaca gtggccagag agggctctgg gcactggagg 60  
 gagcgtcttc ttcctgcca ggggtccctg ggccgatggg atcacgcaga agaatgcgag 120  
 agaagcagcc tttgagaagg gaagtcacta tcccagagcc cagactgagc gg atg gag 178  
 Met Glu  
 1  
 ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga 226  
 Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly  
 5 10 15  
 gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag 274  
 Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu  
 20 25 30  
 ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca 322  
 Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser  
 35 40 45 50  
 cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc 370  
 Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu  
 55 60 65  
 ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac 418  
 Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp  
 70 75 80

tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc	466
Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe	
85 90 95	
gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt ctg ctg ggg	514
Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu Leu Gly	
100 105 110	
ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc cgg cgg aca	562
Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg Arg Thr	
115 120 125 130	
gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct gta gca gac	610
Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val Ala Asp	
135 140 145	
acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac gct gcc gtc	658
Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala Ala Val	
150 155 160	
cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt gcc ctc ttc	706
Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala Leu Phe	
165 170 175	
aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc atc agc ttt	754
Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile Ser Phe	
180 185 190	
gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac cgc cgg ggg	802
Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg Arg Gly	
195 200 205 210	
ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg ggg ctc tgc	850
Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly Leu Cys	
215 220 225	
ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tgc gcc cac cac gac	898
Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His His Asp	
230 235 240	
gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca cag gtg ggc	946
Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln Val Gly	
245 250 255	
cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt ctg ctg ccc	994
Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu Leu Pro	
260 265 270	
ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc gtg ctg ctg	1042
Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val Leu Leu	
275 280 285 290	
gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg gtg gtg gtg	1090
Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val Val Val	
295 300 305	
gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac ctg gtg gtg	1138
Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu Val Val	
310 315 320	



ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc 1186  
 Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly  
 325 330 335

cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc 1234  
 Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly  
 340 345 350

tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc 1282  
 Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val  
 355 360 365 370

aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc 1330  
 Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro  
 375 380 385

aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca 1378  
 Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser  
 390 395 400

tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga 1420  
 Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu  
 405 410 415

ggccggaatc cgggctcccc ttctgcccac agtctgactt ccccgcatte caggctcctc 1480

cctccctctg ccggctctgg ctctcccaa tatcctcgct ccggggactc actggcagcc 1540

ccagcaccac caggtctccc gggaagccac cctcccagct ctgaggactg caccattgct 1600

gctccttagc tgccaagccc catcctgccg cccgaggtgg ctgcctggag cccactgcc 1660

cttctcattt ggaaactaaa acttcatctt cccaagtgc ggggagtaca aggcattggc 1720

tagaggggtgc tgcccatga agccacagcc caggcctcca gctcagcagt gactgtggcc 1780

atgggtccca agacctctat atttgggtctt ttatttttat gtctaaaatc ctgcttaaaa 1840

cttttcaata aacaagatcg tcaggaaaaa aaaaaa 1876

<210> 2

<211> 415

<212> PRT

<213> Homo sapiens

<400> 2

Met Glu Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile  
 1 5 10 15

Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr  
 20 25 30

Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro  
 35 40 45

Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala  
 50 55 60

Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu  
 65 70 75 80

Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu  
 85 90 95

Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu  
 100 105 110

Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg  
 115 120 125

Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val  
 130 135 140

Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala  
 145 150 155 160

Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala  
 165 170 175

Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile  
 180 185 190

Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg  
 195 200 205

Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly  
 210 215 220

Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His  
 225 230 235 240

His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln  
 245 250 255

Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu  
 260 265 270

Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val  
 275 280 285

Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val  
 290 295 300

Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu  
 305 310 315 320

Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn  
 325 330 335

Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly  
 340 345 350

Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val  
 355 360 365

Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly  
 370 375 380

Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg  
 385 390 395 400

Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu  
 405 410 415

<210> 3  
 <211> 29  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains a BamHI restriction enzyme site

<400> 3  
 cgggatacctc catggagttg aggaagtac

29

<210> 4  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains complementary sequences to a BamHI site

<400> 4  
 ggcggatccc gctcacaagc ccgagtagga

30

<210> 5  
 <211> 34  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains a HindIII site  
  
 <400> 5  
 gtccaagctt gccaccatgg agttgaggaa gtac 34  
  
 <210> 6  
 <211> 57  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains complementary sequences to a XhoI site, translation stop  
 codon, and an HA tag  
  
 <400> 6  
 ctgctcgagt caagcgtagt ctgggacgtc gtatgggtag cacaagcccg agtagga 57  
  
 <210> 7  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains a BamHI restriction enzyme site followed by 5 nucleotide  
 s resembling an efficient signal for the initiation of translatio  
 n in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M  
 .)  
  
 <400> 7  
 cgggatccct cccatggagt tgaggaagta c 31  
  
 <210> 8  
 <211> 29  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains the cleavage site for the restriction endonuclease BamHI  
  
 <400> 8  
 cgggatcccg ctcacaagcc cgagtagga 29  
  
 <210> 9  
 <211> 353  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 9  
  
 Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser Asn  
 1 5 10 15

Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro  
 20 25 30  
 Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile  
 35 40 45  
 Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met  
 50 55 60  
 Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr  
 65 70 75 80  
 Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro  
 85 90 95  
 Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu  
 100 105 110  
 Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile  
 115 120 125  
 Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His  
 130 135 140  
 Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile Cys  
 145 150 155 160  
 Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu Leu  
 165 170 175  
 Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr Glu  
 180 185 190  
 Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile Leu  
 195 200 205  
 Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe Cys  
 210 215 220  
 Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys  
 225 230 235 240  
 His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu  
 245 250 255

D2  
 cont.

Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg  
260 265 270

Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp Arg  
275 280 285

Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu Asn  
290 295 300

Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu Leu  
305 310 315 320

Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro Lys  
325 330 335

Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser Thr  
340 345 350

Thr

D<sup>2</sup>  
cond.

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

**DECLARATION OF MELANIE LENHART UNDER 37 C.F.R. § 1.132**

I, Melanie Lenhart, hereby declare and state as follows:

1. I am employed by Human Genome Sciences, Inc. ("HGS"), Rockville, Maryland, as a Manager in the PreClinical Discovery department. Since I began working at HGS in 1995, my duties have primarily included carrying out and analyzing, as both a bench scientist and a manager, extensive DNA sequencing.

2. A partially redacted copy of the American Type Culture Collection ("ATCC") deposit receipt for Deposit Number 97334 is attached hereto as Exhibit A. As the deposit receipt indicates, ATCC Deposit Number 97334 contains a DNA plasmid assigned to the HGS Code Number 498,333, also known within HGS as HGS Clone ID HSATU68. I requested from the ATCC a sample of ATCC Deposit Number 97334 by a purchase order numbered 81449 dated March 13, 2001, a copy of which is attached hereto as Exhibit B. I received the sample of ATCC Deposit Number 97334 from the ATCC in April of 2001, as evidenced by Sales Order # S0241638 from the ATCC, a copy of which is attached hereto as Exhibit C.

3. I have been shown what has been presented to me as Figures 1A-1D as originally filed in the above-captioned patent application (hereinafter "original Figures

1A-1D”), a copy of which original Figures 1A-1D is attached hereto as Exhibit D. I used the nucleotide sequence of HSATU68, as shown in original Figures 1A-1D, as a reference to compare to the nucleotide sequence of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334.

4. A sample of ATCC Deposit Number 97334 was thoroughly sequenced under my supervision in my laboratory at HGS using sequencing methods which were routine and well known in the art prior to January 11, 1996. Exhibit E depicts an alignment of the nucleotide sequence of the deposited clone with the nucleotide sequence shown in original Figures 1A-1D.

5. The nucleotide sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at position 491. More particularly, original Figures 1A-1D show an A residue at position 491, while a T residue is present in the sequence obtained from the DNA clone contained in ATCC Deposit Number 97334.

6. As a result of the above difference at position 491 of the nucleotide sequence, the encoded amino acid sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at the 107<sup>th</sup> codon. More particularly, the 107<sup>th</sup> codon of the nucleotide sequence in original Figures 1A-1D shows an AAC, encoding for an Asn, which differs from the TAC sequence, encoding for a Tyr, deduced from the DNA clone contained in ATCC Deposit Number 97334.

7. The differences in the nucleotide and encoded amino acid sequences noted in paragraphs 5-6 above have been adjusted in the version of Figures 1A-1D attached hereto as Exhibit F. Exhibit G is a marked up version of original Figures 1A-1D showing in red ink the changes made. The nucleotide sequence shown in Exhibit G is identical at



all but one nucleotide to that shown in original Figures 1A-1D; the amino acid sequence shown in Exhibit F is identical at all but one amino acid residue to that shown in original Figures 1A-1D, with the same start codon, stop codon, and length.

8. Based on the experiments described above and the high degree of similarity between the nucleotide and amino acid sequences of original Figures 1A-1D and the corresponding sequences of the deposited clone as shown in Exhibits E, it is my belief that a person of ordinary skill in the art, upon routine sequencing of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334 using methods well known in the art prior to January 11, 1996, would readily determine that the residue at position 491 is an A residue; and thus, the encoded amino acid at position 107 is Tyr, especially when using original Figures 1A-1D as a guide.

9. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date: 3/14/02

Melanie Lenhart  
Melanie Lenhart